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                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                         cis/trans
                                                                  peptidylproline
 terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
                                                                                 (Omega=0).

SUBCELLULAR LOCATION: Nuclear.

SIMILARITY: Belongs to the ppiC/parvulin rotamase family
SIMILARITY: Contains 1 WW domain.

SIMILARITY: Contains 1 WW domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nuclear protein; Rotama
activity. Displays a preference for an acidic residue N-to the isomerized proline bond. Catalyzing pSer/Thr-Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
                                                                  (omega=180)
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7.9e-46;
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 601052; -.
GO; GO: 0005634; C: nucleus; TAS.
GO; GO: 0005515; F: protein binding; TAS.
GO; GO: 0007088; P: regulation of mitosis; TAS.
InterPro; IPR000297; Rotamase.
InterPro; IPR001202; WW_R8p5_WWP.
                                          isomerizations.
CATALYTIC ACTIVITY: Peptidylproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interproj iffondial iffondial interproj iffond
                                                                                                                                                                                                                                                                                                                                                                               EMBL; U49070; AAC50492.1; -
EMBL; BC002899; AAH02899.1;
                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S68520; S68520.
PDB; 1F8A; X-ray; B=1-163.
PDB; 116C; NMR; A=6-44.
PDB; 118H; NMR; B=6-44.
PDB; 118H; NMR; B=6-44.
PDB; 1NMV; NMR; A=1-163.
PDB; 1PIN; X-ray; A=1-163.
Genew; HGNC: 8988; PIN1.
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MIM; 601052; -.
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名かって、より
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=CS7BL/6J, TISSUB=Embryo, and Kidney;

STRAIN=CS7BL/6J, TISSUB=Embryo, and Kidney;

STRAIN=CS7BL/6J, TISSUB=Embryo, and Kidney;

STRAIN=CS7BL/6J, TISSUB=Bmbryo, and Kidney;

NEDDINE=222546683; Pubmed=12466851; DOI=10.1038/nature01266;

Nikaido I., Osato N., Saito R., Adachi J., Bonoo H., Kondo S.,

Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Sadi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

Balde J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Blake J.A., Radioni A., Fletcher C.F., Forrest A., Gough J.,

Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,

Ranai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Radjott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

Ravasi T., Reed J.C., Reed D.J., Ring B.Z., Ringwald M.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Namara R., Taskenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

Namara R., Taskenaka T., Konno H., Nakamura M., Yang I., Yang L.,

Shiraki T., Waki K., Kawai J., Alzawa K., Arakawa T., Rouno H., Nakamura M., Sakazume Pu, Sakai K.,

Sandi A., Hashizume W., Imotani K., Ishiia Y., Itoh M., Kagawa I.,

Namaraki T., Waki K., Kawai J., Shibata K., Shiraki B.,

Namaraki A., Hashizume W., Imotani K., Ishiia Y., Ishida E.S., Roqers J.,

Namaraki T., Waki K., Kawai D., Shibata E.S., Roqers J.,

Namaraki T., Waki R., K., Sasaki D., Shibata S., Shogers J.,
                                                118
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cis/trans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Essential PPIase that regulates mitosis presumably by interacting with NIMA and attenuating its mitosis-promoting activity. Displays a preference for an acidic residue N-terminal to the isomerized proline bond. Catalyzing pSer/Thr-Pro cis/trans
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                                                                                                                                                                                                                                                                                                                                                          .1.8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=20070807; PubMed=10600477; DOI=10.1006/bbrc.1999.1736;
Fujimori F., Takahashi K., Uchida C., Uchida T.;
"Mice lacking Pin1 develop normally, but are defective in entering cell cycle from G0 arrest.";
Biochem. Biophys. Res. Commun. 265:658-663(1999).
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Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                    eostomi
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SUBCELLULAR LOCATION: Nuclear (By similarity).
SIMILARITY: Belongs to the ppiC/parvulin rotamase family
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                                                                                      ч
                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Peptidyl-prolyl cis-trans isomerase NIMA-interacting (Rotamase FIN1) (PPIase Pin1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata, Vertebrata, E
Sciurognathi, Muridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isomerizations (By similarity). CATALYTIC ACTIVITY: Peptidylproline (omega=180)
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Rodentia;
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Nature 420:563-573(2002)
                                                                                                                                                                                                                                                STANDARD;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                musculus
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Q9QUR7;
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Gaps

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163;

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Score 534; D Pred. No. 7.9 ; Mismatches

100.08;

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Query .Match

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                      duced through a collaboration a and the EMBL outstation are no restrictions on its its content is in no way
                                                                     commercial
                                                                     nd for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                     61 HLLVKHSQSRRPSSWRQEKITRSKEEALELINGYIQKIKSGEEDFESLASQFSDCSSAKA
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein (Fragment).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopodinae; Xenopus.
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Clifton
                                                                    and
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Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clit
Richardson P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell proliferation; IMP
                                                                                                                                                                                                                                                                                                                                                                             Length
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PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.(
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M.,
                                                                                                                                                                                                                                                                                                                                             PpiC.
188E95F009176B1F CRC64;
                                                                                                                                                                                                                              InterPro; IPRUUIZUZ; www.kabc_......

Pfam; PF00639; Rotamase; 1.

Pfam; PF00397; WW; 1.

SMART; SM00456; WW; 1.

PROSITE; PS01096; PPIC_PPIASE_1; 1.

PROSITE; PS01159; WW DOMAIN_1; 1.

PROSITE; PS50020; WW DOMAIN_2; 1.

PROSITE; PS50020; WW DOMAIN_2; 1.

Cell cycle; Isomerase; Nuclear protein; Rotamase.

DOMAIN 5 39 WW.

SQUENCE 165 AA; 18370 MW; 188E95F009176B1F CRC
                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                             Score 525; DB 1;
Pred. No. 6.5e-45;
1; Mismatches 1
     domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                  EMBL; AB009691; BAA87037.1; -.
EMBL; AB009692; BAA87038.1; -.
EMBL; AK003369; BAB22743.1; -.
EMBL; AK002665; BAB22270.1; -.
PIR; JC7136; JC7136.
HSSP; Q13526; 1F8A.
MGD; MGI:1346036; Pin1.
GO; GO:0042127; P:regulation of cellinterPro; IPR000297; Rotamase.
InterPro; IPR001202; WW_RSPS_WWP.
                                                                                                                                                                                                                                                                                                                                                                                                     1;
      Contains 1 WW
                                                                                                                                                                                                                                                                                                                                                                               98.3%;
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                                                                                                                                                                                                                                                                                                                                                                                            Similarity 98.3
3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A
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       SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genetic and initiative.";
                                                                                                                                                                                                                                                                                                                                                                                                 93
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E
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Best Local
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Q6AZR5;
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,
Anitialon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Aniting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rrzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=20165035; PubMed=10698738; DOI=10.1126/science.287.5458.1644;
Winkler K.E., Swenson K.I., Kornbluth S., Means A.R.;
"Requirement of the prolyl isomerase Pin1 for the replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Lung;

Klein S., Strausberg R.;

Klein S., Strausberg R.;

Klein S., Strausberg R.;

L. Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

C.:- SIMILARITY: Belongs to the ppiC/parvulin rotamase family.

R EMBL; BC077447; AAH77447.1; -.

R GO; GO:0016853; F:isomerase activity; IEA.

R GO; GO:0016853; F:isomerase.

R InterPro; IPR002349; WW.

R InterPro; IPR001202; WW.Rsp5_WWP.

R InterPro; IPR001202; WW.Rsp5_WWP.

Pfam; PF00639; Rotamase; 1.

DR Pfam; PF006397; WW; 1.

PRINTS; PR00403; WWDOMAIN.

SMART; SM00456; WW; 1.
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Last sequence update)
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Pred. No. 5.3e-41
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00456; WW; 1.
PROSITE; PS01096; PPIC PPIASE 1; 1.
PROSITE; PS50198; PPIC PPIASE 2; 1.
PROSITE; PS01159; WW DOMAIN 1; 1.
PROSITE; PS50020; WW DOMAIN 2; 1.
Hypothetical protein; Isomerase; Rotamase.
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Similarity 88.6%;
93; Conservative
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